REMARKS

Reconsideration and allowance are respectfully requested.

Claims 34-42 and 46 are pending in the application with Claim 34 being the sole independent claim.

Applicants respectfully request a signed copy of the IDS submitted April 27, 2001 for their files.

Turning to the Office Action mailed December 19, 2003:

Claims 34-42, and 46 have been rejected under **35 U.S.C. § 101** and **35 U.S.C. §112, first paragraph**. Applicants respectfully traverse. Applicants respectfully submit that there is no reason to doubt that the amino acid sequence of SEQ ID NO:6 has 3-dehydroquinate synthase activity, based on percent identity to a reference protein. Regardless, see also the attached Appendix A. Appendix A corresponds to the first page of a BLASTP analysis performed June 7, 1999, using the amino acid sequence derived from clone se3.pk0029.f9:fis1 (SEQ ID NO:6) as a query against the NCBI database. Furthermore, two specific and substantial utilities for the polypeptides of the invention are described in the specification at page 10, lines 26-30 and page 1, lines 18 and 19.

Claims 34-42, and 46 have been rejected under **35 U.S.C. §112, first paragraph**, as allegedly not being enabled. Applicants respectfully traverse.

Applicants previous remarks in the response filed February 26, 2003 are incorporated here again.

One of ordinary skill in the art can combine the specification with the teachings of *both* Bischoff et al. *and* of Carpenter et al., which Applicants submit are *within the knowledge of one of ordinary skill in the art*, to determine polynucleotides encoding a polypeptide having 3-dehydroquinate synthase activity, wherein the amino acid sequence of the polypeptide is at least 90% identical to the amino acid sequence having SEQ ID NO:6. Bischoff et al. demonstrated that an *L. esculentum* 3-dehydroquinate synthase was capable of complementing a strain of *E. coli* that is deficient in such enzyme, even though the *E. coli* 3-dehydroquinate synthase is *only 52.2% identical* to the *L. esculentum* enzyme. Carpenter et al. teach nine key amino acids involved in critical interactions in the proposed 3-dehydroquinate synthase catalytic mechanism. One of ordinary skill in the art, in view of both of these teachings, can identify which amino acids can and cannot be changed in an amino acid sequence having at least 90% identity to SEQ ID NO:6, while still retaining 3-dehyroquinate synthase activity.

Applicants believe the foregoing to be responsive to each of the points raised in the Office Action. Early and favorable notification of allowance is hereby solicited.

Please charge any fees associated with the filing of this response, including but not limited to the Extension of Time, to Deposit Account No. 04-1928 (E. I. du Pont the Nemours and Company). If the fee is insufficient or incorrect, please charge or credit the balance to the above-identified deposit account.

Respectfully submitted,

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Dated: June 21, 2004

APPENDIX A

BLASTP 2.0.8 [Jan-05-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= se3.pk0029.f9.fis1 6/7/99 no filter, Becky
(437 letters)

Database: /blast/data/2.0/2/nr
380,262 sequences; 116,472,368 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value	pLog
gi|114181|sp|P07639|AROB_ECOLI 3-DEHYDROQUINATE SYNTHASE >gi|683...	368	e-101	101.00
gi|3023329|sp|P77980|AROB_SALTY 3-DEHYDROQUINATE SYNTHASE >gi|16...	363	1e-99	
gi|1168503|sp|P43879|AROB_HAEIN 3-DEHYDROQUINATE SYNTHASE >gi|10...	349	2e-95	
gi|3913105|sp|O50468|AROB_NEIGO 3-DEHYDROQUINATE SYNTHASE >gi|26...	348	4e-95	
gi|3913106|sp|P73997|AROB_SYNY3 3-DEHYDROQUINATE SYNTHASE >gi|16...	272	5e-72	
gi|399057|sp|P31102|AROB_BACSU 3-DEHYDROQUINATE SYNTHASE >gi|143...	238	6e-62	
gi|2492962|sp|P56081|AROB_HELPY 3-DEHYDROQUINATE SYNTHASE >gi|23...	211	9e-54	
gi|98800|pir||S17768 3-dehydroquinate synthase (EC 4.6.1.3) - My...	210	2e-53	
gi|3915615|sp|P36919|AROB_MYCTU 3-DEHYDROQUINATE SYNTHASE >gi|17...	210	2e-53	
gi|4154792 (AE001464) 3-DEHYDROQUINATE SYNTHASE [Helicobacter py...	208	5e-53	

>gi|114181|sp|P07639|AROB_ECOLI 3-DEHYDROQUINATE SYNTHASE >gi|68385|pir||SYECQ 3-dehydroquinate
synthase (EC 4.6.1.3) - Escherichia coli
>gi|40968|emb|CAA27495| (X03867) 3-dehydroquinate
synthase (aa 1-362) [Escherichia coli]
>gi|41225|emb|CAA79666| (Z19601) ORF, aroB. Millar G.,
Coggins J.R.; FEBS Lett. 200:11-17(1986) [Escherichia
coli] >gi|606323 (U18997) 3-dehydroquinate synthase
[Escherichia coli] >gi|1789791 (AE000414)
3-dehydroquinate synthase [Escherichia coli]
Length = 362

Score = 368 bits (935), Expect = e-101
Identities = 191/333 (57%), Positives = 234/333 (69%), Gaps = 2/333 (0%)

```
Query: 76  VEVDLGSRSYPIYIGSGLLNQPDYLQRHVHGKRVLVVTNETVAPLYLDKVVDALTRGNPN 135
           + V LG RSYPI I SGL N+P         G++V++VTNET+APLYLDKV    L +
Sbjct: 4   IVVTLGERSYPITIASGLFNEPASFLPLKSGEQVMLVTNETLAPLYLDKVRGVLEQAG-- 61

Query: 136 VSVESVILPDGEQYKDMDTLMKVFDKAIESRLDRRCTFVALGGGVIGDMCGFAASAFLRG 195
           V+V+SVILPDGEQYK +  L  VF   ++    R  T VALGGGV+GD+ GFAA+++ RG
Sbjct: 62  VNVDSVILPDGEQYKSLAVLDTVFTALLQKPHGRDTTLVALGGGVVGDLTGFAAASYQRG 121

Query: 196 VNFIQIPTTVMAQVDSSVGGKTGINHRLGKNMIGTFYQPQCVLIDTDTLNTLPDRELASG 255
           V FIQ+PTT+++QVDSSVGGKT +NH LGKNMIG FYQP  V++D D L TLP RELASG
Sbjct: 122 VRFIQVPTTLLSQVDSSVGGKTAVNHPLGKNMIGAFYQPASVVVDLDCLKTLPPRELASG 181

Query: 256 LAEVIKYGLIRDAEFFEWQEKNMHLLLARDPSVMAYAIKRSCENKAEVVSLDQKESGLRA 315
           LAEVIKYG+I D   FF W E+N+  LL  D   MAY I+R CE KAEVV+ D++E+GLRA
Sbjct: 182 LAEVIKYGIILDGAFFNWLEENLDALLRLDGPAMAYCIRRCCELKAEVVAADERETGLRA 241

Query: 316 TLNLGHTFGHAIETGVGYGQWLHGEAVAAGTVMAVDMSYRLGWIDDSLVKRVGDILKQAK 375
            LNLGHTFGHAIE  +GYG WLHGEAVAAG VMA   S RLG    +  +R+  +LK+A
Sbjct: 242 LLNLGHTFGHAIEAEMGYGNWLHGEAVAAGMVMAARTSERLGQFSSAETQRIITLLKRAG 301

Query: 376 LPTAPPETVTVDMFKSVMAVDKKVADGLLRLIL 408
           LP   P  ++   +   M  DKKV  G +RLIL
Sbjct: 302 LPVNGPREMSAQAYLPHMLRDKKVLAGEMRLIL 334
```